

SEQUENCE LISTING

<110> Wong, Justin
 Winter, Jill
 Lalehzadeh, Guita
 Warne, Robert

<120> Compositions and Methods of Therapy for
 Cancers Characterized by Expression of the Tumor-Associated
 Antigen MN/CA IX

<130> PP19155.003

<150> 60/405,577

<151> 2002-08-23

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1380)

<400> 1

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1 5 10 15	
cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg	96
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu	
20 25 30	
atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gat tcc ccc	144
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro	
35 40 45	
ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat	192
Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp	
50 55 60	
ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag	240
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu	
65 70 75 80	
gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct	288
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro	
85 90 95	
gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat	336
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp	
100 105 110	
cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat	384
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn	
115 120 125	
gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg cgc tat gga	432
Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly	
130 135 140	

ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc	480
Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe	
145 150 155 160	
cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc	528
Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala	
165 170 175	
ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa	576
Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu	
180 185 190	
ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc ctg cct cct	624
Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro	
195 200 205	
ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg gct ctg cag	672
Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln	
210 215 220	
ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg gag cac act	720
Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr	
225 230 235 240	
gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc	768
Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser	
245 250 255	
acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg	816
Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu	
260 265 270	
gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc	864
Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala	
275 280 285	
tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca	912
Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser	
290 295 300	
gag act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac	960
Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp	
305 310 315 320	
ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt	1008
Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys	
325 330 335	
gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt	1056
Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser	
340 345 350	
gct aag cag ctc cac acc ctc tct gac acc ctg tgg gga cct ggt gac	1104
Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp	
355 360 365	
tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg aat ggg cga	1152
Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg	
370 375 380	
gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt cct cgg gct	1200
Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala	
385 390 395 400	

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gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt gac atc cta 1248
Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
          405          410          415

gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt 1296
Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
          420          425          430

gtg cag atg aga agg cag cac aga agg gga acc aaa ggg ggt gtg agc 1344
Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
          435          440          445

tac cgc cca gca gag gta gcc gag act gga gcc tag 1380
Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala *
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<210> 2
<211> 459
<212> PRT
<213> Homo sapiens

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 20          25          30
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
 35          40          45
Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
 50          55          60
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
 65          70          75          80
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
 85          90          95
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
100          105          110
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
115          120          125
Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
130          135          140
Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
145          150          155          160
Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
165          170          175
Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
180          185          190
Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
195          200          205
Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
210          215          220
Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
225          230          235          240
Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
245          250          255
Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
260          265          270
Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
275          280          285
Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
290          295          300
Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
305          310          315          320
Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
325          330          335
Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser

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          340          345          350
Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
          355          360          365
Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
          370          375          380
Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
          385          390          395          400
Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
          405          410          415
Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
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Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
          435          440          445
Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
          450          455

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<210> 3
 <211> 540
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Coding sequence for human CA IX proteoglycan
 domain construct

<221> CDS
 <222> (1)...(540)

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ctt gct cca ggc ctc act gtg caa ctg ctg tca ctg ctg ctt ctg 96
Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Ser Leu Leu Leu
20 25 30

atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gat tcc ccc 144
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
35 40 45

ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat 192
Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
50 55 60

ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag 240
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
65 70 75 80

gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct 288
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
85 90 95

gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat 336
Glu Val Lys Pro Lys Ser Glu Glu Gly Ser Leu Lys Leu Glu Asp
100 105 110

cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat 384
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
115 120 125

gcc cat agg agc tcg agc atc cta gcc ctg gtt ttt ggc ctc ctt ttt 432

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Ala His Arg Ser Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe
 130                      135                      140

gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag cac aga   480
Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg
145                      150                      155                      160

agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta gcc gag   528
Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu
                      165                      170                      175

act gga gcc tag   :   540
Thr Gly Ala  *

```

<210> 4
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Polypeptide encoded by coding sequence for human
 CA IX proteoglycan domain construct

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<400> 4
Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
 1                      5                      10                      15
Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
                      20                      25                      30
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
                      35                      40                      45
Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
50                      55                      60
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
65                      70                      75                      80
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
                      85                      90                      95
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
                      100                     105                     110
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
                      115                     120                     125
Ala His Arg Ser Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe
130                      135                      140
Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg
145                      150                      155                      160
Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu
                      165                      170                      175
Thr Gly Ala

```

<210> 5
 <211> 1089
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Coding sequence for human CA IX carbonic anhydrase
 domain construct

<221> CDS
 <222> (1)...(1089)

<400> 5

atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg atc ccg gcc	48
Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala	
1 5 10 15	
cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg	96
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu	
20 25 30	
atg cct gtc cat ccc ggg gat gac cag agt cat tgg cgc tat gga ggc	144
Met Pro Val His Pro Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly	
35 40 45	
gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc cag	192
Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln	
50 55 60	
tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc ctg	240
Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu	
65 70 75 80	
cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa ctg	288
Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu	
85 90 95	
cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc ctg cct cct ggg	336
Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly	
100 105 110	
cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg	384
Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu	
115 120 125	
cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg	432
His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val	
130 135 140	
gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc acc	480
Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr	
145 150 155 160	
gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc	528
Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala	
165 170 175	
gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat	576
Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr	
180 185 190	
gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca gag	624
Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu	
195 200 205	
act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac ttc	672
Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe	
210 215 220	
agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt gcc	720
Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala	
225 230 235 240	
cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt gct	768
Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala	
245 250 255	

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aag cag ctc cac acc ctc tct gac acc ctg tgg gga cct ggt gac tct      816
Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser
                260                      265                  270

cgg cta cag ctg aac ttc cga gcg acg cag cct ttg aat ggg cga gtg      864
Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val
                275                      280                  285

att gag gcc tcc ttc cct gct gga gtg gac agc agt cct cgg gct gct      912
Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala
                290                      295                  300

gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt gac atc cta gcc      960
Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala
305                      310                      315                  320

ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg      1008
Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val
                325                      330                  335

cag atg aga agg cag cac aga agg gga acc aaa ggg ggt gtg agc tac      1056
Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr
                340                      345                  350

cgc cca gca gag gta gcc gag act gga gcc tag                          1089
Arg Pro Ala Glu Val Ala Glu Thr Gly Ala *
                355                      360

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<210> 6

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide encoded by coding sequence for human
CA IX carbonic anhydrase domain construct

<400> 6

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Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
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Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Ser Leu Leu Leu
 20          25          30
Met Pro Val His Pro Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly
 35          40          45
Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln
 50          55          60
Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu
 65          70          75          80
Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu
 85          90          95
Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly
 100         105         110
Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu
 115         120         125
His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val
 130         135         140
Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr
 145         150         155         160
Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala
 165         170         175
Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr
 180         185         190
Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu
 195         200         205

```

```

Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe
210                215                220
Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala
225                230                235                240
Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala
                245                250                255
Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser
                260                265                270
Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val
                275                280                285
Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala
290                295                300
Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala
305                310                315                320
Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val
                325                330                335
Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr
                340                345                350
Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
                355                360

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<210> 7
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Coding sequence for glu-tagged human CA IX
 carbonic anhydrase domain construct

<221> CDS
 <222> (1)...(978)

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<400> 7
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Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
1                5                10                15

cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg 96
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
                20                25                30

atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gct agc gaa 144
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Ala Ser Glu
                35                40                45

tac atg cca atg gaa caa gaa ccc cag aat aat gcc cac agg gac aaa 192
Tyr Met Pro Met Glu Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
                50                55                60

gaa ggg gat gac cag agt cat tgg cgc tat gga ggc gac ccg ccc tgg 240
Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
65                70                75                80

ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc cag tcc ccg gtg gat 288
Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
                85                90                95

atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc ctg cgc ccc ctg gaa 336
Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
                100                105                110

ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa ctg cgc ctg cgc aac 384

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Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn	
		115					120					125				
aat	ggc	cac	agt	gtg	caa	ctg	acc	ctg	cct	cct	ggg	cta	gag	atg	gct	432
Asn	Gly	His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	Gly	Leu	Glu	Met	Ala	
		130				135					140					
ctg	ggc	ccc	ggg	cgg	gag	tac	cgg	gct	ctg	cag	ctg	cat	ctg	cac	tgg	480
Leu	Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	His	Leu	His	Trp	
		145			150					155					160	
ggg	gct	gca	ggc	cgt	ccg	ggc	tgc	gag	cac	act	gtg	gaa	ggc	cac	cgt	528
Gly	Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg	
				165					170					175		
ttc	cct	gcc	gag	atc	cac	gtg	gtt	cac	ctc	agc	acc	gcc	ttt	gcc	aga	576
Phe	Pro	Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg	
			180					185					190			
gtt	gac	gag	gcc	ttg	ggg	cgc	ccg	gga	ggc	ctg	gcc	gtg	ttg	gcc	gcc	624
Val	Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala	
		195					200					205				
ttt	ctg	gag	gag	ggc	ccg	gaa	gaa	aac	agt	gcc	tat	gag	ctc	cac	acc	672
Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Leu	His	Thr	
		210				215					220					
ctc	tct	gac	acc	ctg	tgg	gga	cct	ggt	gac	tct	cgg	cta	cag	ctg	aac	720
Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu	Asn	
		225			230					235					240	
ttc	cga	gcg	acg	cag	cct	ttg	aat	ggg	cga	gtg	att	gag	gcc	tcc	ttc	768
Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser	Phe	
				245					250					255		
cct	gct	gga	gtg	gac	agc	agt	cct	cgg	gct	gct	gag	cca	gtc	cag	ctg	816
Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala	Glu	Pro	Val	Gln	Leu	
			260					265					270			
aat	tcc	tgc	ctg	gct	gct	ggc	gac	atc	cta	gcc	ctg	gtt	ttt	ggc	ctc	864
Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp	Ile	Leu	Ala	Leu	Val	Phe	Gly	Leu	
		275					280					285				
ctt	ttt	gct	gtc	acc	agc	gtc	gcg	ttc	ctt	gtg	cag	atg	aga	agg	cag	912
Leu	Phe	Ala	Val	Thr	Ser	Val	Ala	Phe	Leu	Val	Gln	Met	Arg	Arg	Gln	
		290				295					300					
cac	aga	agg	gga	acc	aaa	ggg	ggt	gtg	agc	tac	cgc	cca	gca	gag	gta	960
His	Arg	Arg	Gly	Thr	Lys	Gly	Gly	Val	Ser	Tyr	Arg	Pro	Ala	Glu	Val	
		305			310				315						320	
gcc	gag	act	gga	gcc	tag											978
Ala	Glu	Thr	Gly	Ala	*											
				325												

<210> 8

<211> 325

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide encoded by coding sequence for
glu-tagged human CA IX carbonic anhydrase domain
construct

<400> 8

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Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
 1          5          10          15
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
 20          25          30
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Ala Ser Glu
 35          40          45
Tyr Met Pro Met Glu Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
 50          55          60
Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
 65          70          75          80
Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
 85          90          95
Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
100          105          110
Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
115          120          125
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
130          135          140
Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
145          150          155          160
Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
165          170          175
Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
180          185          190
Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
195          200          205
Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr
210          215          220
Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn
225          230          235          240
Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe
245          250          255

Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu
260          265          270
Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu
275          280          285
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln
290          295          300
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val
305          310          315          320
Ala Glu Thr Gly Ala
325

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<210> 9

<211> 978

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for glu-tagged mutant human CA IX
carbonic anhydrase domain construct

<221> CDS

<222> (1)...(978)

<400> 9

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atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg atc ccg gcc 48
Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
 1          5          10          15

cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg 96
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu

```

20						25						30						
atg	cct	gtc	cat	ccc	cag	agg	ttg	ccc	cgg	atg	cag	gag	gct	agc	gaa	144		
Met	Pro	Val	His	Pro	Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Ala	Ser	Glu			
35						40						45						
tac	atg	cca	atg	gaa	caa	gaa	ccc	cag	aat	aat	gcc	cac	agg	gac	aaa	192		
Tyr	Met	Pro	Met	Glu	Gln	Glu	Pro	Gln	Asn	Asn	Ala	His	Arg	Asp	Lys			
50						55						60						
gaa	ggg	gat	gac	cag	agt	cat	tgg	cgc	tat	gga	ggc	gac	ccg	ccc	tgg	240		
Glu	Gly	Asp	Asp	Gln	Ser	His	Trp	Arg	Tyr	Gly	Gly	Asp	Pro	Pro	Trp			
65						70						75			80			
ccc	cgg	gtg	tcc	cca	gcc	tgc	gcg	ggc	cgc	ttc	cag	tcc	ccg	gtg	gat	288		
Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	Gln	Ser	Pro	Val	Asp			
			85						90						95			
atc	cgc	ccc	cag	ctc	gcc	gcc	ttc	tgc	ccg	gcc	ctg	cgc	ccc	ctg	gaa	336		
Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu			
			100						105						110			
ctc	ctg	ggc	ttc	cag	ctc	ccg	ccg	ctc	cca	gaa	ctg	cgc	ctg	cgc	aac	384		
Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn			
			115						120						125			
aat	ggc	cac	agt	gtg	caa	ctg	acc	ctg	cct	cct	ggg	cta	gag	atg	gct	432		
Asn	Gly	His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	Gly	Leu	Glu	Met	Ala			
			130			135						140						
ctg	ggt	ccc	ggg	cgg	gag	tac	cgg	gct	ctg	cag	ctg	caa	ctg	cag	tgg	480		
Leu	Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	Gln	Leu	Gln	Trp			
145						150						155			160			
ggg	gct	gca	ggt	cgt	ccg	ggc	tcg	gag	cac	act	gtg	gaa	ggc	cac	cgt	528		
Gly	Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg			
			165						170						175			
ttc	cct	gcc	gag	atc	caa	gtg	gtt	cac	ctc	agc	acc	gcc	ttt	gcc	aga	576		
Phe	Pro	Ala	Glu	Ile	Gln	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg			
			180						185						190			
gtt	gac	gag	gcc	ttg	ggg	cgc	ccg	gga	ggc	ctg	gcc	gtg	ttg	gcc	gcc	624		
Val	Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala			
			195						200						205			
ttt	ctg	gag	gag	ggc	ccg	gaa	gaa	aac	agt	gcc	tat	gag	ctc	cac	acc	672		
Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Leu	His	Thr			
			210			215						220						
ctc	tct	gac	acc	ctg	tgg	gga	cct	ggt	gac	tct	cgg	cta	cag	ctg	aac	720		
Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu	Asn			
225						230						235			240			
ttc	cga	gcg	acg	cag	cct	ttg	aat	ggg	cga	gtg	att	gag	gcc	tcc	ttc	768		
Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser	Phe			
			245						250						255			
cct	gct	gga	gtg	gac	agc	agt	cct	cgg	gct	gct	gag	cca	gtc	cag	ctg	816		
Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala	Glu	Pro	Val	Gln	Leu			
			260						265						270			
aat	tcc	tgc	ctg	gct	gct	ggt	gac	atc	cta	gcc	ctg	gtt	ttt	ggc	ctc	864		
Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp	Ile	Leu	Ala	Leu	Val	Phe	Gly	Leu			
			275			280						285						

```

ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag 912
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln
290 295 300

```

```

cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta 960
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val
305 310 315 320

```

```

gcc gag act gga gcc tag 978
Ala Glu Thr Gly Ala *
325

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<210> 10
<211> 325
<212> PRT
<213> Artificial Sequence

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<220>
<223> Polypeptide encoded by coding sequence for
glu-tagged mutant human CA IX carbonic anhydrase
domain construct

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<400> 10
Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
1 5 10 15
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu
20 25 30
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Ala Ser Glu
35 40 45
Tyr Met Pro Met Glu Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
50 55 60
Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Asp Pro Pro Trp
65 70 75 80
Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
85 90 95
Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
100 105 110
Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
115 120 125
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
130 135 140
Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu Gln Leu Trp
145 150 155 160
Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
165 170 175
Phe Pro Ala Glu Ile Gln Val Val His Leu Ser Thr Ala Phe Ala Arg
180 185 190
Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
195 200 205
Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr
210 215 220
Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn
225 230 235 240
Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe
245 250 255
Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu
260 265 270
Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu
275 280 285
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln
290 295 300
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val
305 310 315 320
Ala Glu Thr Gly Ala
325

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